

WO 01/18047

PCT/AU00/01083

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SEQUENCE LISTING

<110> The Council of the Queensland Institute of Medical Research

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Lys Asp Val Ser Tyr Cys Arg Asn Lys Ile Gly Thr Tyr Ile Cys Ser
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Ala Gly Asn Asn Thr Met Lys Val Asp Cys Thr Ser Gly Phe Lys Glu
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His Asn Ser Gly Gly Glu Thr Ala Val Ala Phe Ile Ala Tyr Lys Ser

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	Phe Leu Cys Ala Asp Val Asp Glu Cys Leu Thr Ile Gly Ile Cys Pro		140
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	Lys Tyr Ser Asn Cys Ser Asn Ser Val Gly Ser Tyr Ser Cys Thr Cys		160
	145	150	155
	Gln Pro Gly Phe Val Leu Asn Gly Ser Ile Cys Glu Asp Glu Asp Glu		175
25	165	170	
	Cys Val Thr Arg Asp Val Cys Pro Glu His Ala Thr Cys His Asn Thr		190
	180	185	190
30	Leu Gly Ser Tyr Tyr Cys Thr Cys Asn Ser Gly Leu Glu Ser Ser Gly		205
	195	200	
	Gly Gly Pro Met Phe Gln Gly Leu Asp Glu Ser Cys Glu Asp Val Asp		220
35	210	215	220
	Glu Cys Ser Arg Asn Ser Thr Leu Cys Gly Pro Thr Phe Ile Cys Ile		240
	225	230	235
	Asn Thr Leu Gly Ser Tyr Ser Cys Ser Cys Pro Ala Gly Phe Ser Leu		255
40	245	250	
	Pro Thr Phe Gln Ile Leu Gly His Pro Ala Asp Gly Asn Cys Thr Asp		270
	260	265	270
45	Ile Asp Glu Cys Asp Asp Thr Cys Pro Leu Asn Ser Ser Cys Thr Asn		285
	275	280	
	Thr Ile Gly Ser Tyr Phe Cys Thr Cys His Pro Gly Phe Ala Ser Ser		300
50	290	295	300
	Asn Gly Gln Leu Asn Phe Lys Asp Leu Glu Val Thr Cys Glu Asp Ile		320
	305	310	315
	Asp Glu Cys Thr Gln Asp Pro Leu Gln Cys Gly Leu Asn Ser Val Cys		335
55	325	330	
	Thr Asn Val Pro Gly Ser Tyr Ile Cys Gly Cys Leu Pro Asp Phe Gln		350
	340	345	350

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	Met	Asp	Pro	Glu	Gly	Ser	Gln	Gly	Tyr	Gly	Asn	Phe	Asn	Cys	Lys	Arg
			355					360					365			
5	Ile	Leu	Phe	Lys	Cys	Lys	Glu	Asp	Leu	Ile	Leu	Gln	Ser	Glu	Gln	Ile
	370						375					380				
	Gln	Gln	Cys	Gln	Ala	Val	Gln	Gly	Arg	Asp	Leu	Gly	Tyr	Ala	Ser	Phe
	385					390					395					400
10	Cys	Thr	Leu	Val	Asn	Ala	Thr	Phe	Thr	Ile	Leu	Asp	Asn	Thr	Cys	Glu
					405					410					415	
	Asn	Lys	Ser	Ala	Pro	Val	Ser	Leu	Gln	Ser	Ala	Ala	Thr	Ser	Val	Ser
15				420					425					430		
	Leu	Val	Leu	Glu	Gln	Ala	Thr	Thr	Trp	Phe	Glu	Leu	Ser	Lys	Glu	Glu
		435						440					445			
20	Thr	Ser	Thr	Leu	Gly	Thr	Ile	Leu	Leu	Glu	Thr	Val	Glu	Ser	Thr	Met
	450						455					460				
	Leu	Ala	Ala	Leu	Leu	Ile	Pro	Ser	Gly	Asn	Ala	Ser	Gln	Met	Ile	Gln
	465					470					475					480
25	Thr	Glu	Tyr	Leu	Asp	Ile	Glu	Ser	Lys	Val	Ile	Asn	Glu	Glu	Cys	Lys
				485						490					495	
	Glu	Asn	Glu	Ser	Ile	Asn	Leu	Ala	Ala	Arg	Gly	Asp	Lys	Met	Asn	Val
30				500					505					510		
	Gly	Cys	Phe	Ile	Ile	Lys	Glu	Ser	Val	Ser	Thr	Gly	Ala	Pro	Gly	Val
			515					520					525			
35	Ala	Phe	Val	Ser	Phe	Ala	His	Met	Glu	Ser	Val	Leu	Asn	Glu	Arg	Phe
	530						535					540				
	Phe	Glu	Asp	Gly	Gln	Ser	Phe	Arg	Lys	Leu	Arg	Met	Asn	Ser	Arg	Val
	545					550				555						560
40	Val	Gly	Gly	Thr	Val	Thr	Gly	Glu	Lys	Lys	Glu	Asp	Phe	Ser	Lys	Pro
				565						570					575	
	Ile	Ile	Tyr	Thr	Leu	Gln	His	Ile	Gln	Pro	Lys	Gln	Lys	Ser	Glu	Arg
45			580						585					590		
	Pro	Ile	Cys	Val	Ser	Trp	Asn	Thr	Asp	Val	Glu	Asp	Gly	Arg	Trp	Thr
		595					600					605				
50	Pro	Ser	Gly	Cys	Glu	Ile	Val	Glu	Ala	Ser	Glu	Thr	His	Thr	Val	Cys
	610						615					620				
	Ser	Cys	Asn	Arg	Met	Ala	Asn	Leu	Ala	Ile	Ile	Met	Ala	Ser	Gly	Glu
	625					630					635					640
55	Leu	Thr	Met	Glu	Phe	Ser	Leu	Tyr	Ile	Ile	Ser	His	Val	Gly	Thr	Val
					645					650					655	

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<213> Homo sapiens

<400> 7

5	Met	Gly	Gly	Arg	Val	Phe	Leu	Ala	Phe	Cys	Val	Trp	Leu	Thr	Leu	Pro	1	5	10	15
	Gly	Ala	Glu	Thr	Gln	Asp	Ser	Arg	Gly	Cys	Ala	Arg	Val	Cys	Pro	Gln	20	25	30	
10	Asn	Ser	Ser	Cys	Val	Asn	Ala	Thr	Ala	Cys	Arg	Cys	Asn	Pro	Gly	Phe	35	40	45	
	Ser	Ser	Phe	Ser	Glu	Ile	Ile	Thr	Thr	Pro	Thr	Glu	Thr	Cys	Asp	Asp	50	55	60	
15	Ile	Asn	Glu	Cys	Ala	Thr	Pro	Ser	Lys	Val	Ser	Cys	Gly	Lys	Phe	Ser	65	70	75	80
	Asp	Cys	Trp	Asn	Thr	Glu	Gly	Ser	Tyr	Asp	Cys	Val	Cys	Ser	Pro	Gly	85	90	95	
20	Tyr	Glu	Pro	Val	Ser	Gly	Ala	Lys	Thr	Phe	Lys	Asn	Glu	Ser	Glu	Asn	100	105	110	
25	Thr	Cys	Gln	Asp	Glu	Cys	Ser	Ser	Gly	Gln	His	Gln	Cys	Asp	Ser	Ser	115	120	125	
	Thr	Val	Cys	Phe	Asn	Thr	Val	Gly	Ser	Tyr	Ser	Cys	Arg	Cys	Arg	Pro	130	135	140	
30	Gly	Trp	Lys	Pro	Arg	His	Gly	Ile	Pro	Asn	Asn	Gln	Lys	Asp	Thr	Val	145	150	155	160
	Cys	Glu	Asp	Met	Thr	Phe	Ser	Thr	Trp	Thr	Pro	Pro	Pro	Gly	Val	His	165	170	175	
35	Ser	Gln	Thr	Leu	Ser	Arg	Phe	Phe	Asp	Lys	Val	Gln	Asp	Leu	Gly	Arg	180	185	190	
40	Asp	Ser	Lys	Thr	Ser	Ser	Ala	Glu	Val	Thr	Ile	Gln	Asn	Val	Ile	Lys	195	200	205	
	Leu	Val	Asp	Glu	Leu	Met	Glu	Ala	Pro	Gly	Asp	Val	Glu	Ala	Leu	Ala	210	215	220	
45	Pro	Pro	Val	Arg	His	Leu	Ile	Ala	Thr	Gln	Leu	Leu	Ser	Asn	Leu	Glu	225	230	235	240
	Asp	Ile	Met	Arg	Ile	Leu	Ala	Lys	Ser	Leu	Pro	Lys	Gly	Pro	Phe	Thr	245	250	255	
50	Tyr	Ile	Ser	Pro	Ser	Asn	Thr	Glu	Leu	Thr	Leu	Met	Ile	Gln	Glu	Arg	260	265	270	
55	Gly	Asp	Lys	Asn	Val	Thr	Met	Gly	Gln	Ser	Ser	Ala	Arg	Met	Lys	Leu	275	280	285	
	Asn	Trp	Ala	Val	Ala	Ala	Gly	Ala	Glu	Asp	Pro	Gly	Pro	Ala	Val	Ala				

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	290	295	300
	Gly Ile Leu Ser Ile Gln Asn Met Thr Thr	Leu Leu Ala Asn Ala Ser	315 320
5	Leu Asn Leu His Ser Lys Lys Gln Ala Glu Leu Glu Glu Ile Tyr Glu		330 335
10	Ser Ser Ile Arg Gly Val Gln Leu Arg Arg Leu Ser Ala Val Asn Ser		340 345 350
15	Ile Phe Leu Ser His Asn Asn Thr Lys Glu Leu Asn Ser Pro Ile Leu		355 360 365
20	Phe Ala Phe Ser His Leu Glu Ser Ser Asp Gly Glu Ala Gly Arg Asp		370 375 380
25	Pro Pro Ala Lys Asp Val Met Pro Gly Pro Arg Gln Glu Leu Leu Cys		385 390 395 400
30	Ala Phe Trp Lys Ser Asp Ser Asp Arg Gly Gly His Trp Ala Thr Glu		405 410 415
35	Val Cys Gln Val Leu Gly Ser Lys Asn Gly Ser Thr Thr Cys Gln Cys		420 425 430
40	Ser His Leu Ser Ser Phe Thr Ile Leu Met Ala His Tyr Asp Val Glu		435 440 445
45	Asp Trp Lys Leu Thr Leu Ile Thr Arg Val Gly Leu Ala Leu Ser Leu		450 455 460
50	Phe Cys Leu Leu Leu Cys Ile Leu Thr Phe Leu Leu Val Arg Pro Ile		465 470 475 480
55	Gln Gly Ser Arg Thr Thr Ile His Leu His Leu Cys Ile Cys Leu Phe		485 490 495
60	Val Gly Ser Thr Ile Phe Leu Ala Gly Ile Glu Asn Glu Gly Gly Gln		500 505 510
65	Val Gly Leu Arg Cys Arg Leu Val Ala Gly Leu Leu His Tyr Cys Phe		515 520 525
70	Leu Ala Ala Phe Cys Trp Met Ser Leu Glu Gly Leu Glu Leu Tyr Phe		530 535 540
75	Leu Val Val Arg Val Phe Gln Gly Gln Gly Leu Ser Thr Arg Trp Leu		545 550 555 560
80	Cys Leu Ile Gly Tyr Gly Val Pro Leu Leu Ile Val Gly Val Ser Ala		565 570 575
85	Ala Ile Tyr Ser Lys Gly Tyr Gly Arg Pro Arg Tyr Cys Trp Leu Asp		580 585 590
90	Phe Glu Gln Gly Phe Leu Trp Ser Phe Leu Gly Pro Val Thr Phe Ile		595 600 605

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Ile Leu Cys Asn Ala Val Ile Phe Val Thr Thr Val Trp Lys Leu Thr
610 615 620

5 Gln Lys Phe Ser Glu Ile Asn Pro Asp Met Lys Lys Leu Lys Lys Ala
625 630 635 640

Arg Ala Leu Thr Ile Thr Ala Ile Ala Gln Leu Phe Leu Leu Gly Cys
645 650 655

10 Thr Trp Val Phe Gly Leu Phe Ile Phe Asp Asp Arg Ser Leu Val Leu
660 665 670

Thr Tyr Val Phe Thr Ile Leu Asn Cys Leu Gln Gly Ala Phe Leu Tyr
675 680 685

15 Leu Leu His Cys Leu Leu Asn Lys Lys Val Arg Glu Glu Tyr Arg Lys
690 695 700

20 Trp Ala Cys Leu Val Ala Gly Gly Ser Lys Tyr Ser Glu Phe Thr Ser
705 710 715 720

Thr Thr Ser Gly Thr Gly His Asn Gln Thr Arg Ala Leu Arg Ala Ser
725 730 735

25 Glu Ser Gly Ile
740

30 <210> 8
<211> 30
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<213> Artificial Sequence

35 <220>
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<400> 8
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40

<210> 9
<211> 32
<212> DNA
<213> Artificial Sequence

45 <220>
<223> Description of Artificial Sequence: PCR primers

50 <400> 9
cgcggaagctt tcaatcttga catttctcat gg 32

55 <210> 10
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<213> Artificial Sequence

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<220>
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 5 gacgggatcc aatgagtgtc tactgaaaga attg 34
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<220>

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32

10

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<211> 20

<212> DNA

<213> Mus musculus

15

<400> 16

cacctgcagc tcttccatct

20

20

<210> 17

<211> 23

<212> DNA

<213> Mus musculus

25

<400> 17

gaaagtttgc ttctcaaaat cca

23

30

<210> 18

<211> 26

<212> DNA

<213> Homo sapiens

35

<400> 18

tgtctcattg cacctcttgg ttccat

26

40

<210> 19

<211> 19

<212> DNA

<213> Homo sapiens

45

<400> 19

ccacaacagc acccactgt

19

50

<210> 20

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<213> Artificial Sequence

55

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33

<210> 21

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10

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15 <213> Artificial Sequence

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